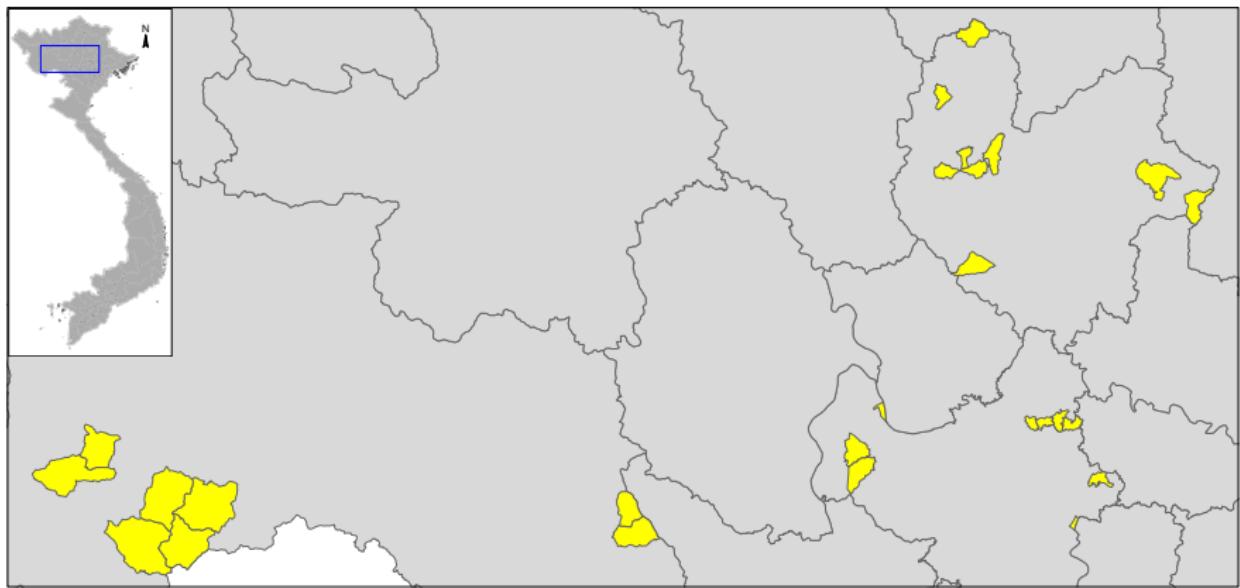
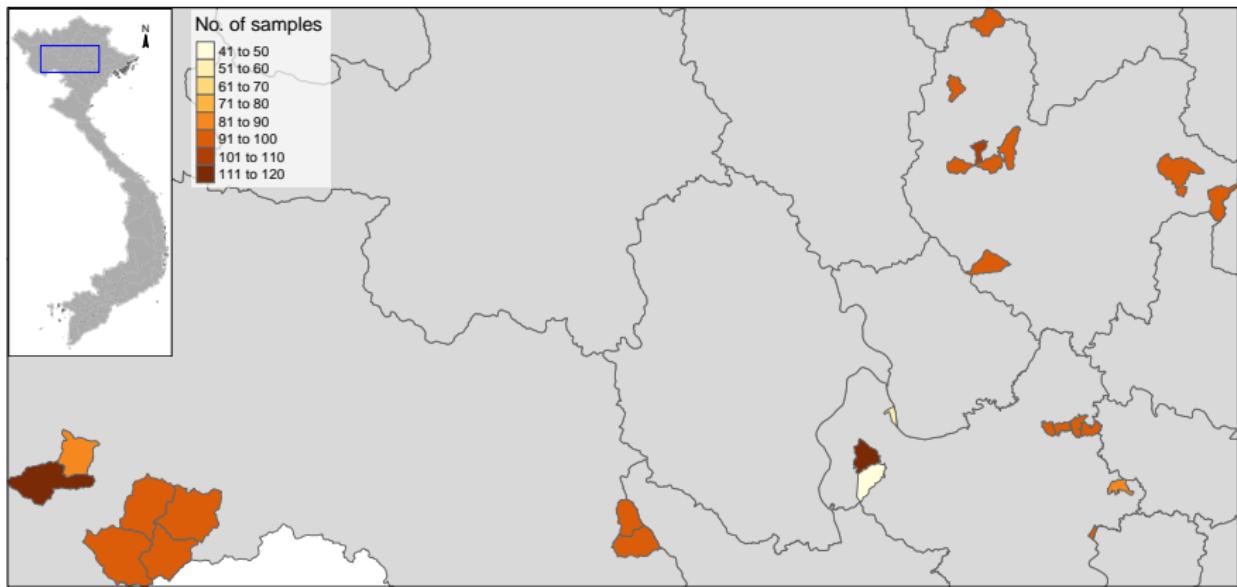


## Preliminary results

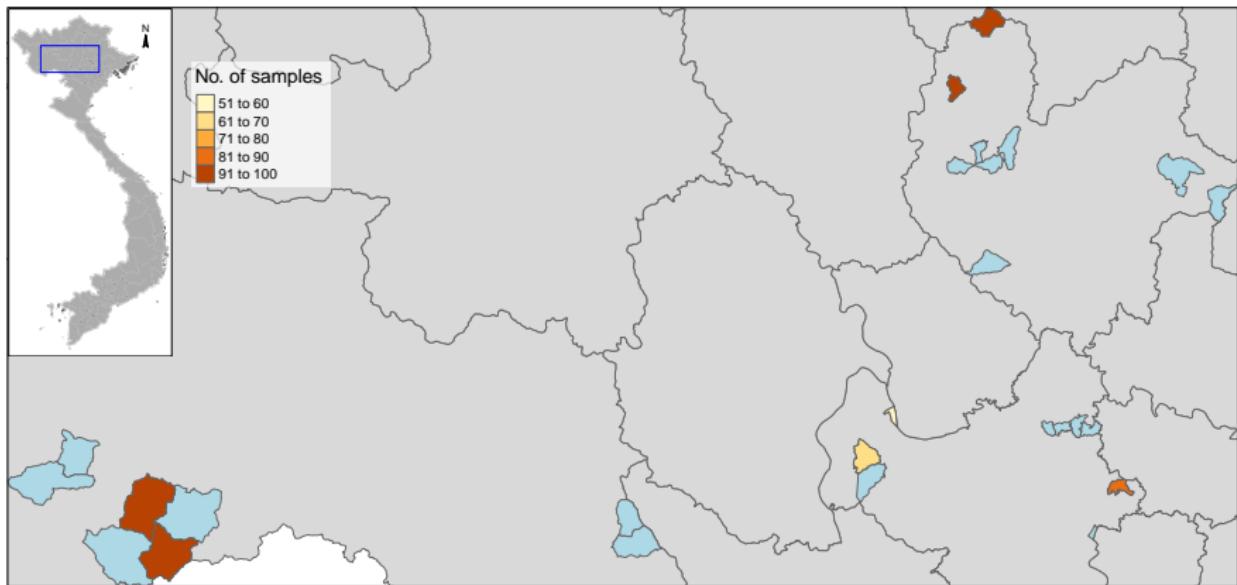
Province	Animal types	summer	autumn	winter	spring
Hà Ni	Buffalo	50	50	49	51
Hà Ni	Cattle	50	50	64	59
Hà Ni	Goat	50	50	41	46
Hà Ni	Horse	50	50	46	44
Sn La	Buffalo	50	50	46	41
Sn La	Cattle	50	50	67	58
Sn La	Goat	50	50	50	60
Sn La	Horse	50	50	37	41
Thái Nguyên	Buffalo	50	50	54	55
Thái Nguyên	Cattle	50	50	57	46
Thái Nguyên	Goat	50	50	51	50
Thái Nguyên	Horse	50	50	38	49



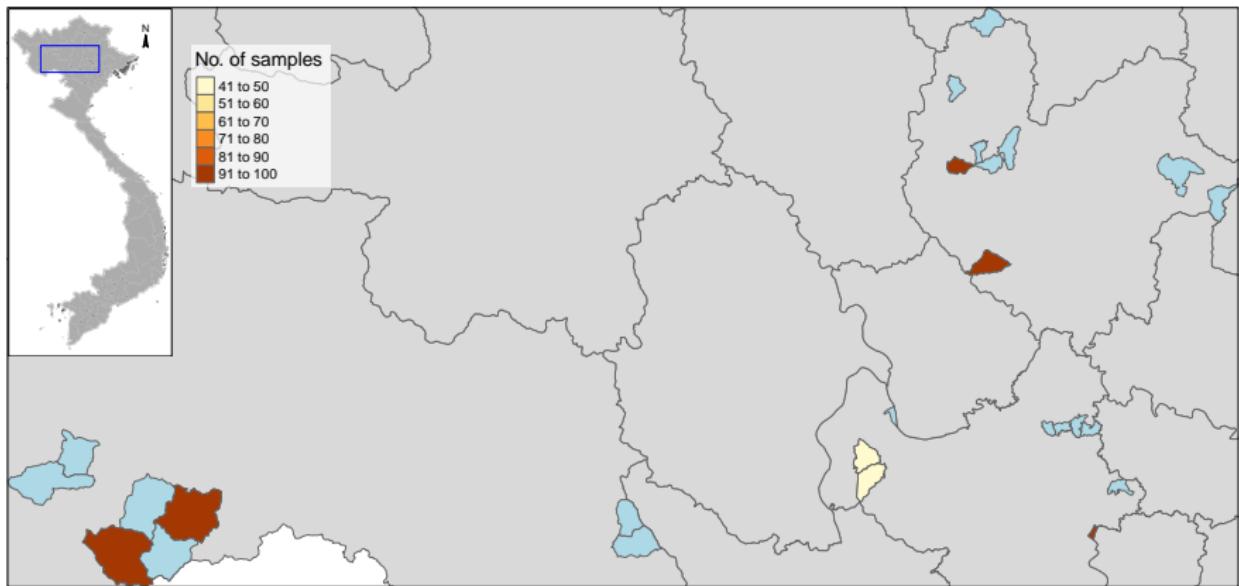
Commune	summer	autumn	winter	spring
Bac Hong	0	0	0	100
Binh Long	0	0	100	0
Cat Ne	0	100	0	0
Chieng Cang	0	100	0	0
Chieng Khoong	100	0	0	0
Chieng So	0	0	0	85
Dong Dat	0	0	0	99
Dong Thinh	100	0	0	0
Duc Luong	0	100	0	0
Hop Thanh	0	0	0	101
Kim Lan	0	100	0	0
Lien Hoa	0	0	100	0
Linh Thong	100	0	0	0
Minh Chau	56	0	0	0
Muong Cai	0	100	0	0
Muong Hung	100	0	0	0
Nam Man	0	0	0	115
Nguyen Khe	0	0	0	100
Phu Dong	82	0	0	0
Song Khua	0	0	100	0
Tan Linh	62	50	0	0
Thuy Lam	0	0	100	0
Trang	0	0	100	0
Van Hoa	0	50	0	0
Xuan Non	0	0	100	0



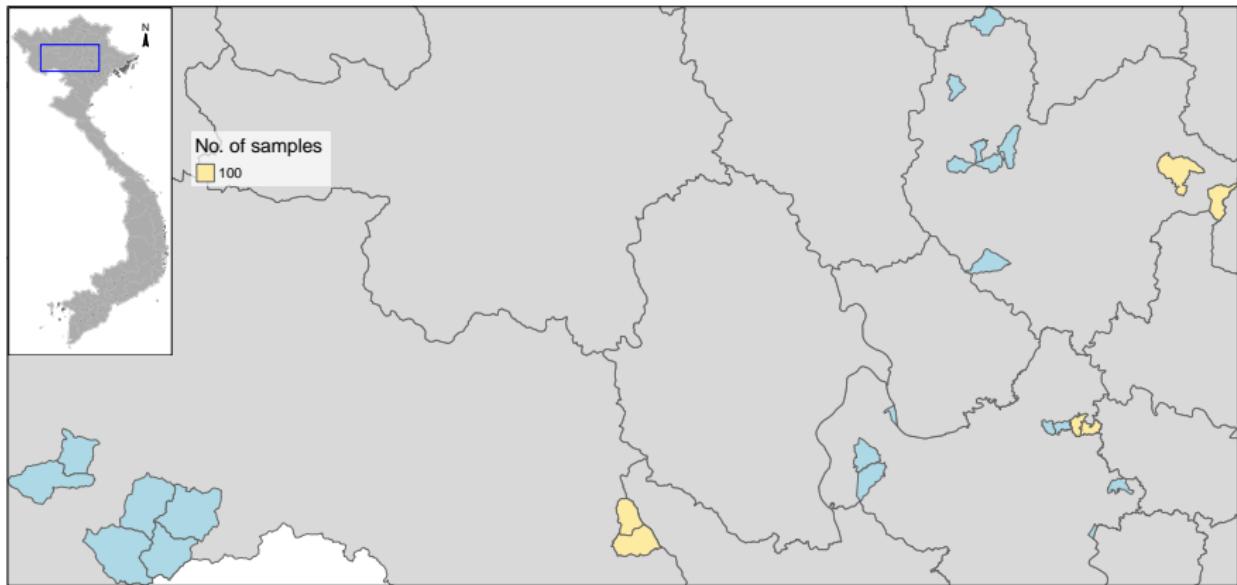
summer



autumn



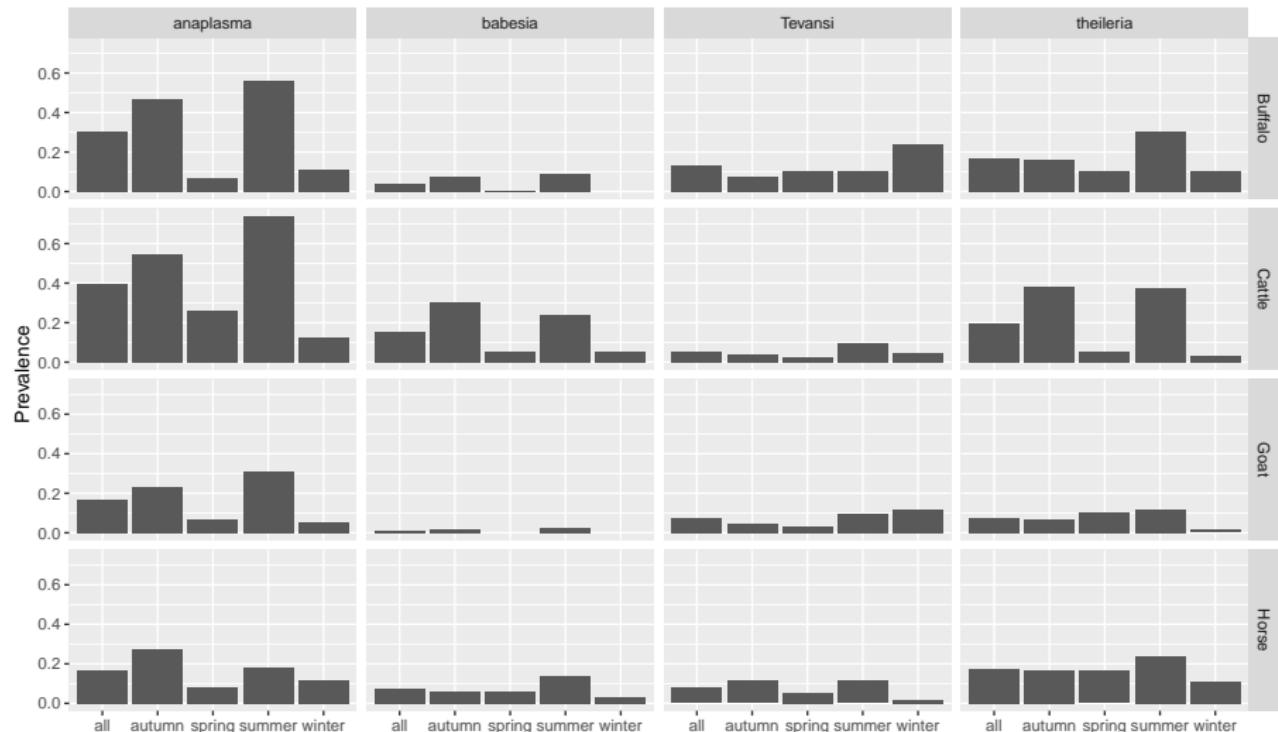
winter

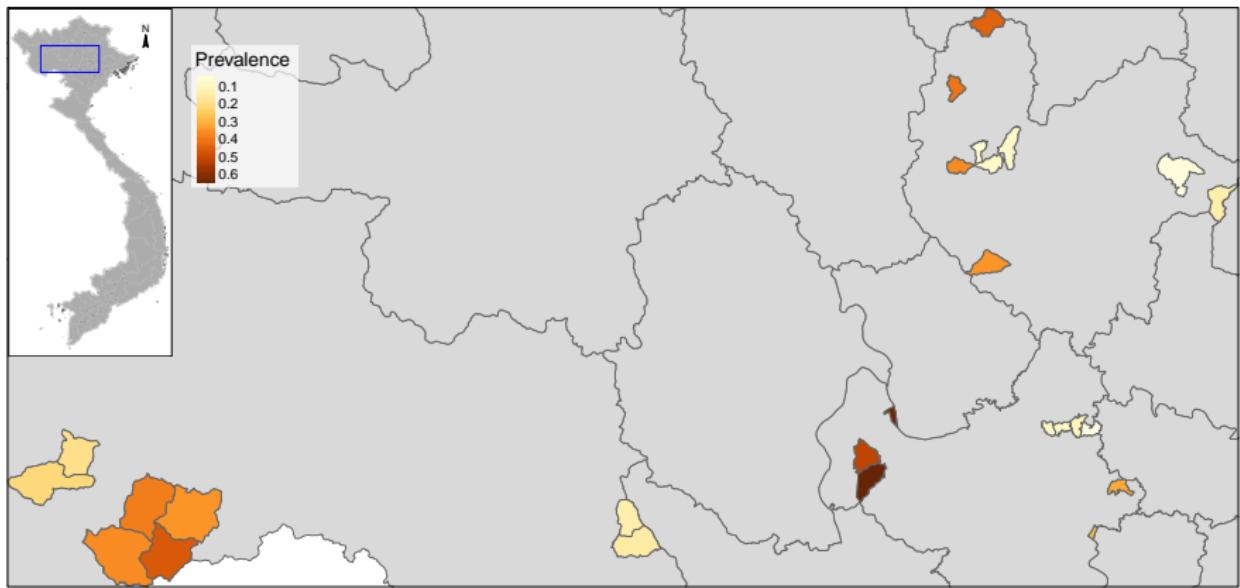


spring

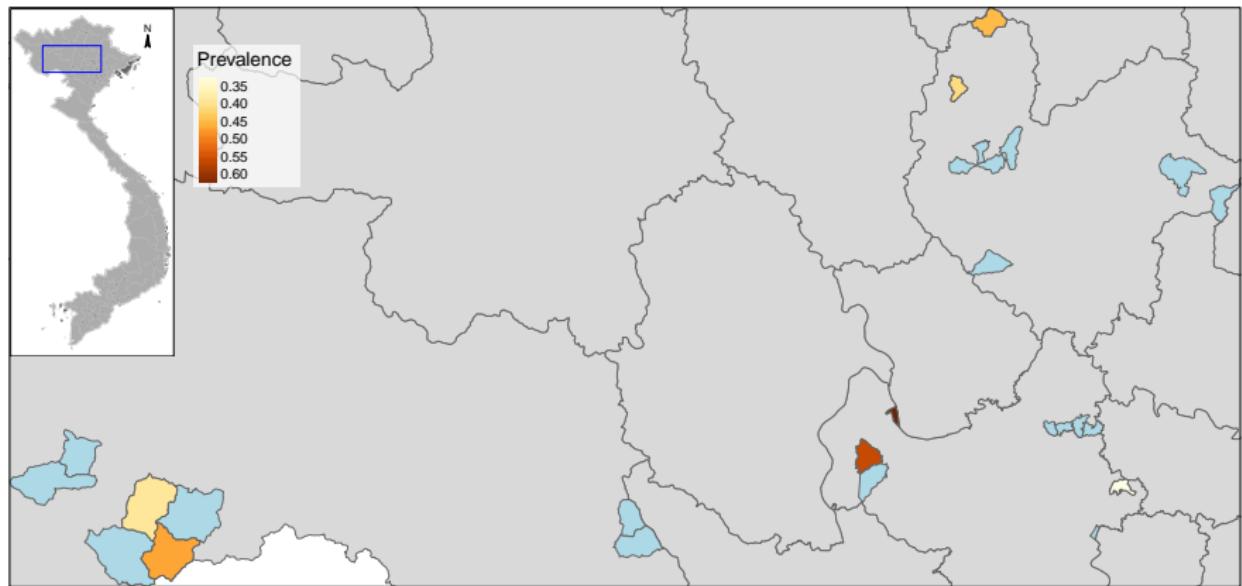


# Prevalence

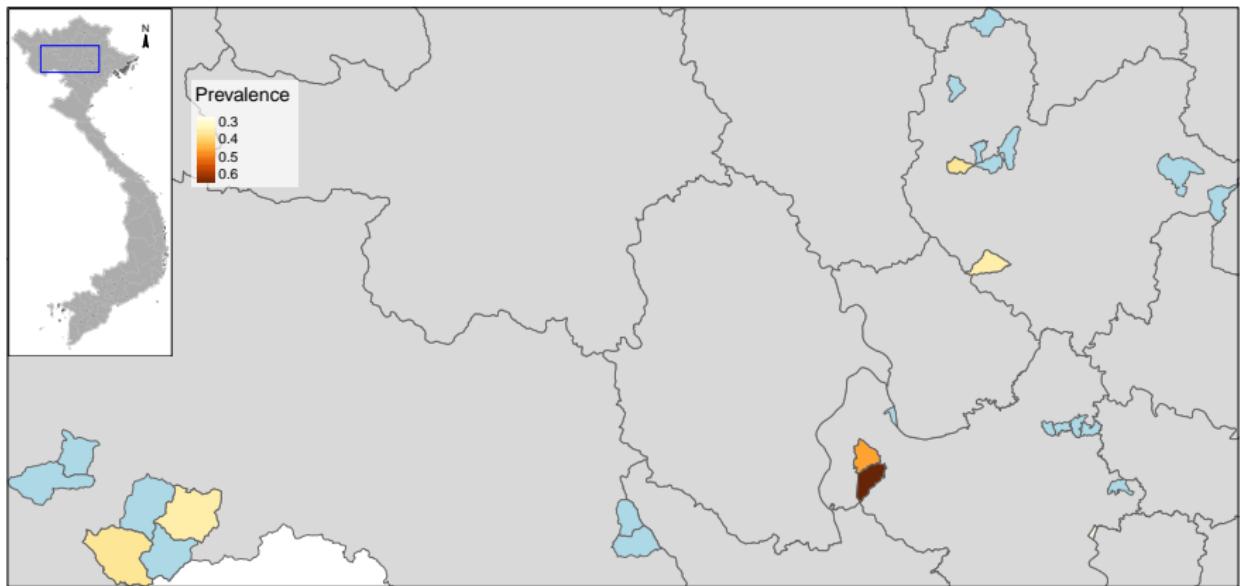




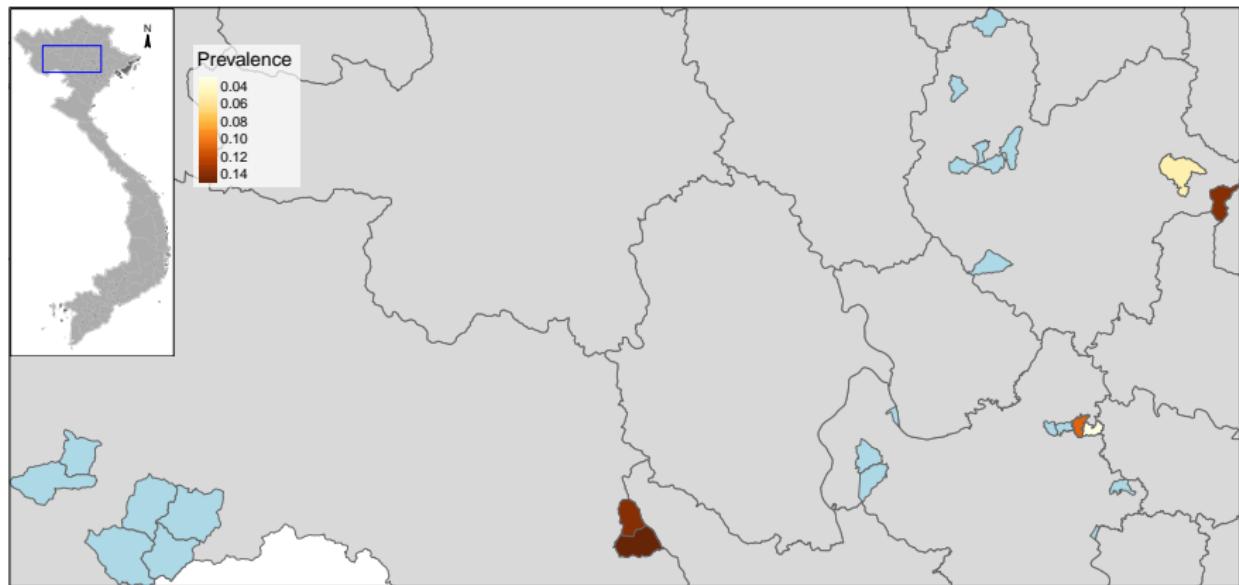
summer



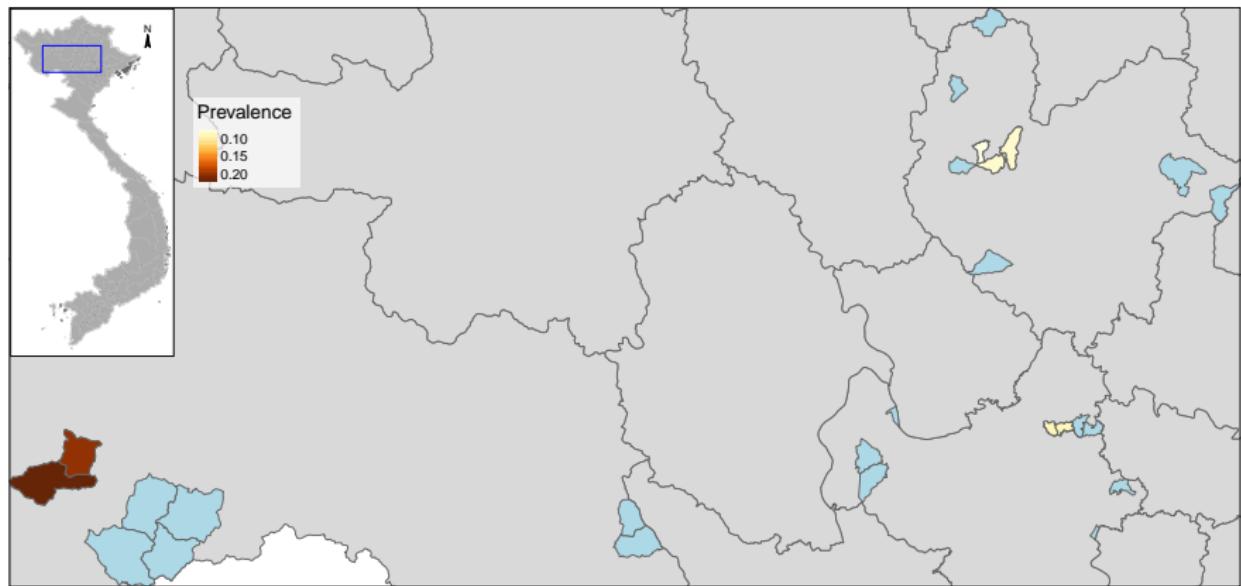
autumn

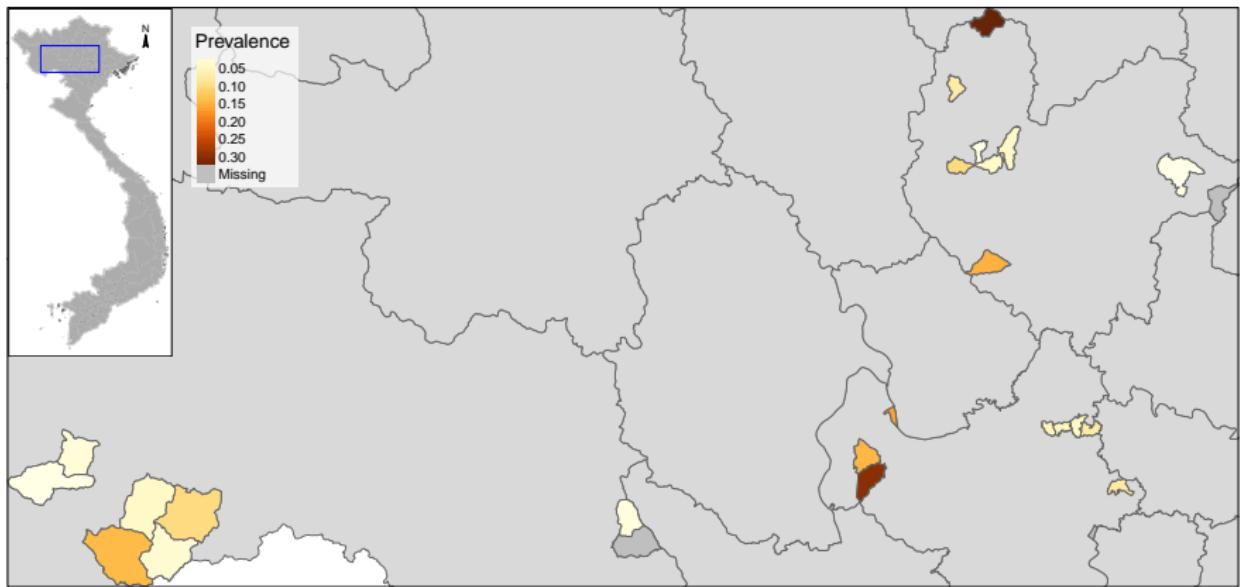


winter

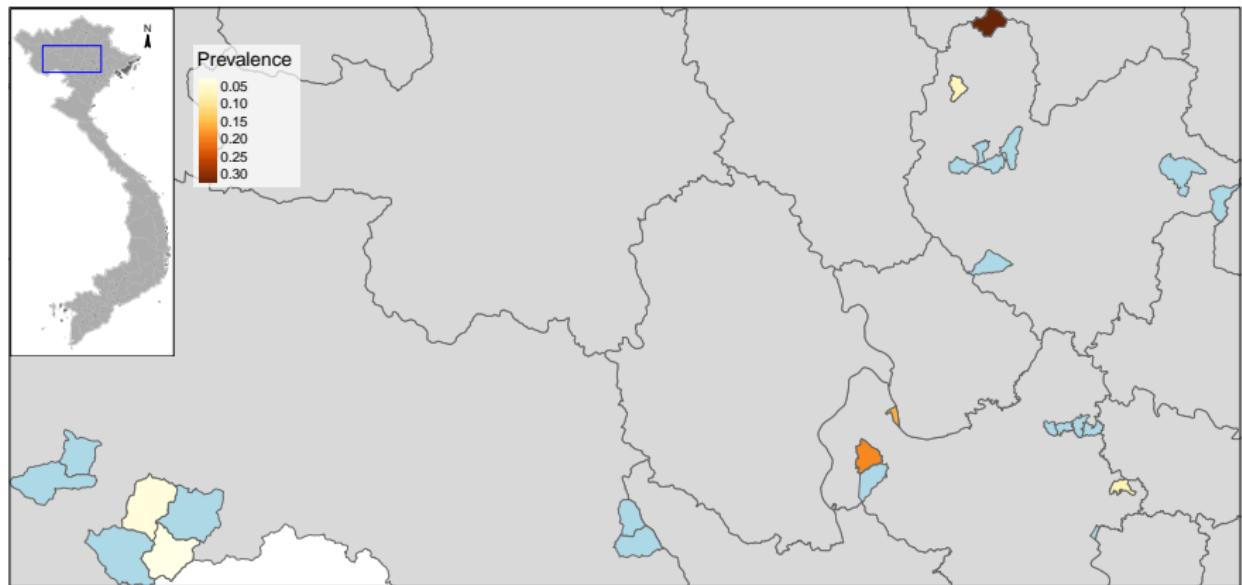


spring





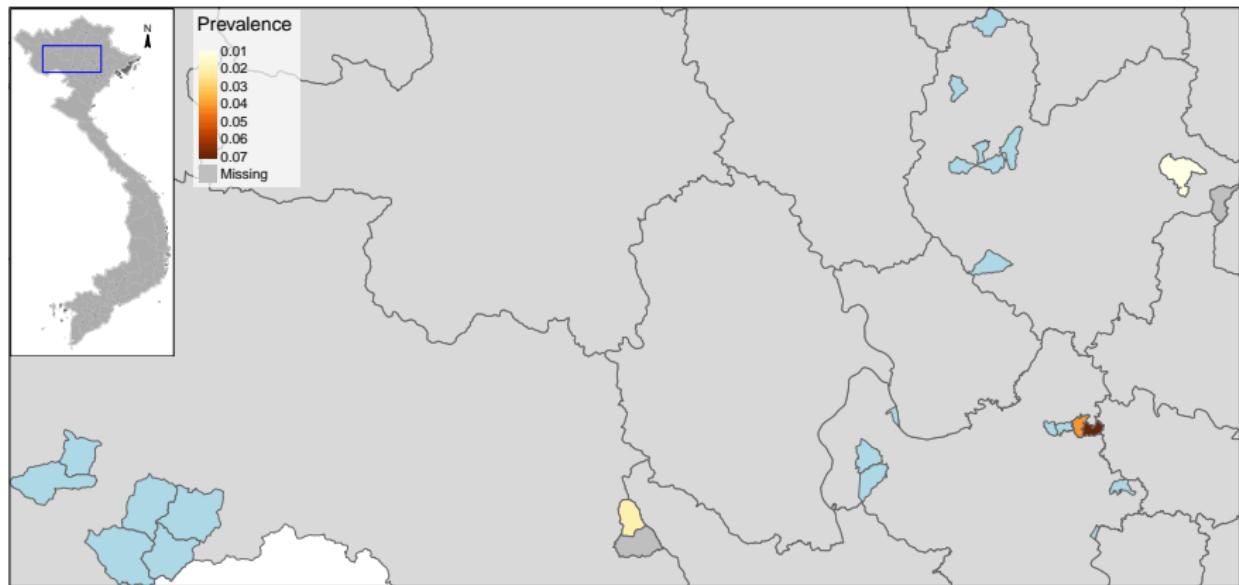
summer



autumn

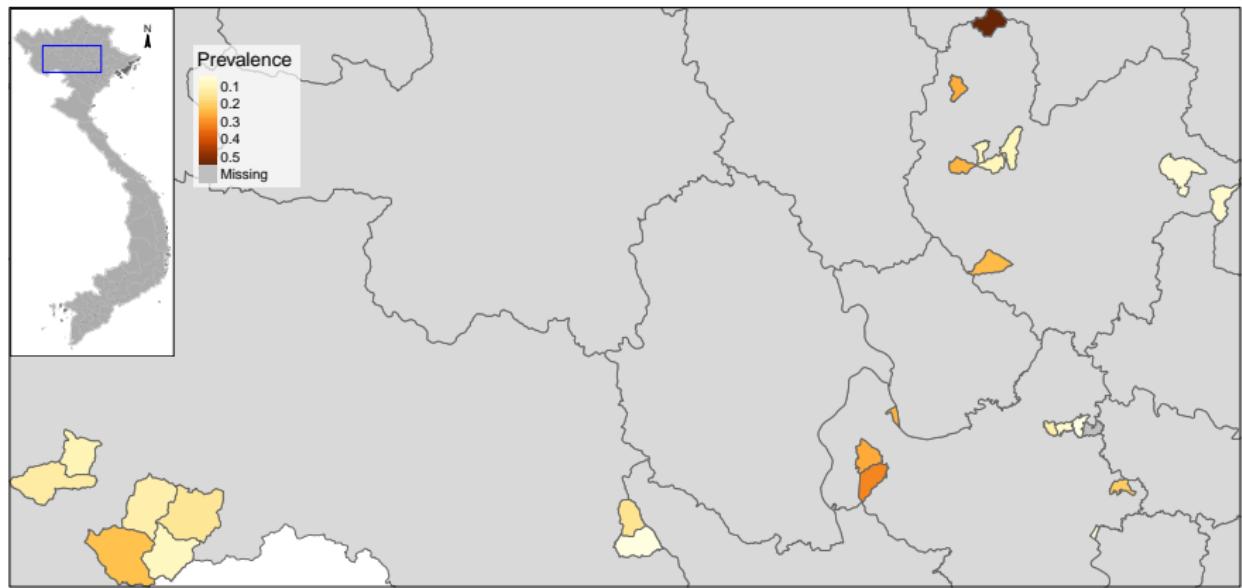


winter

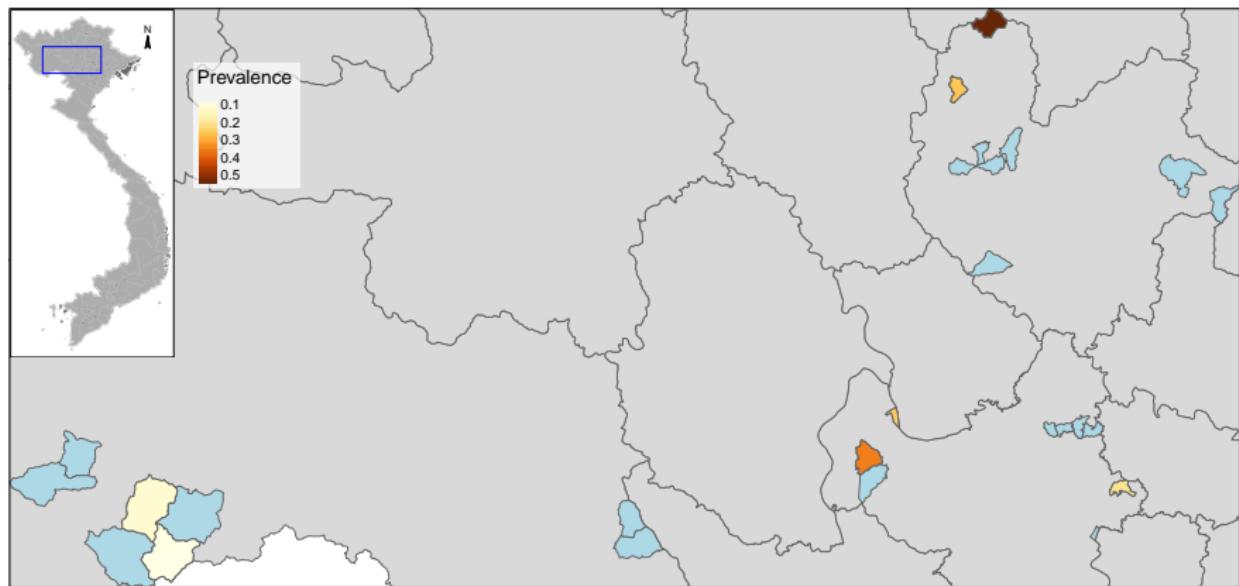


spring





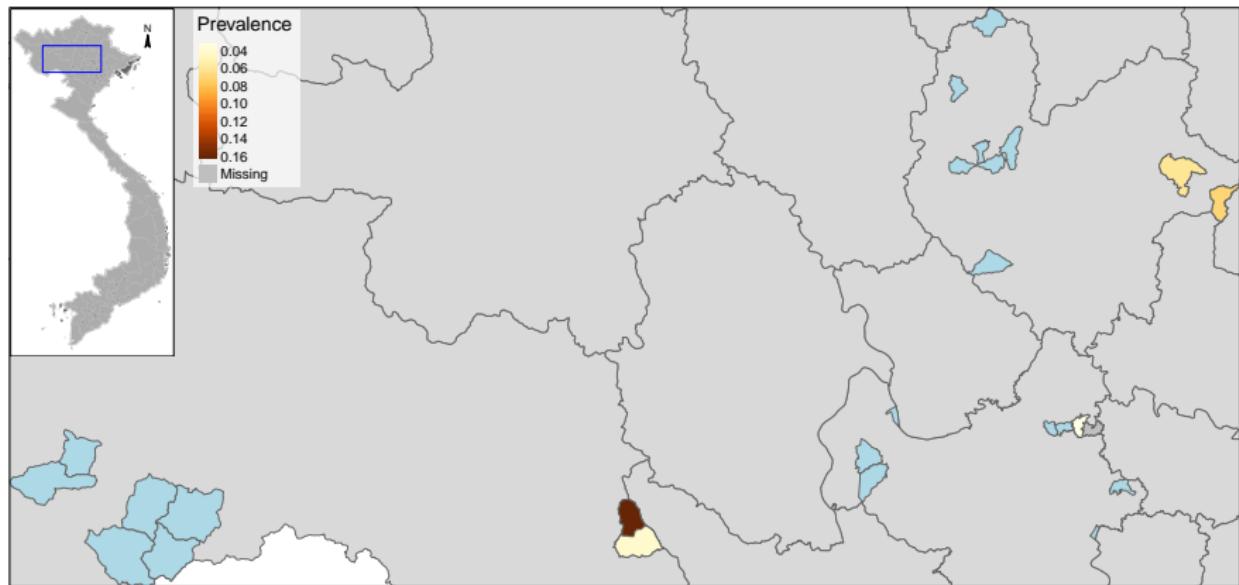
summer



autumn

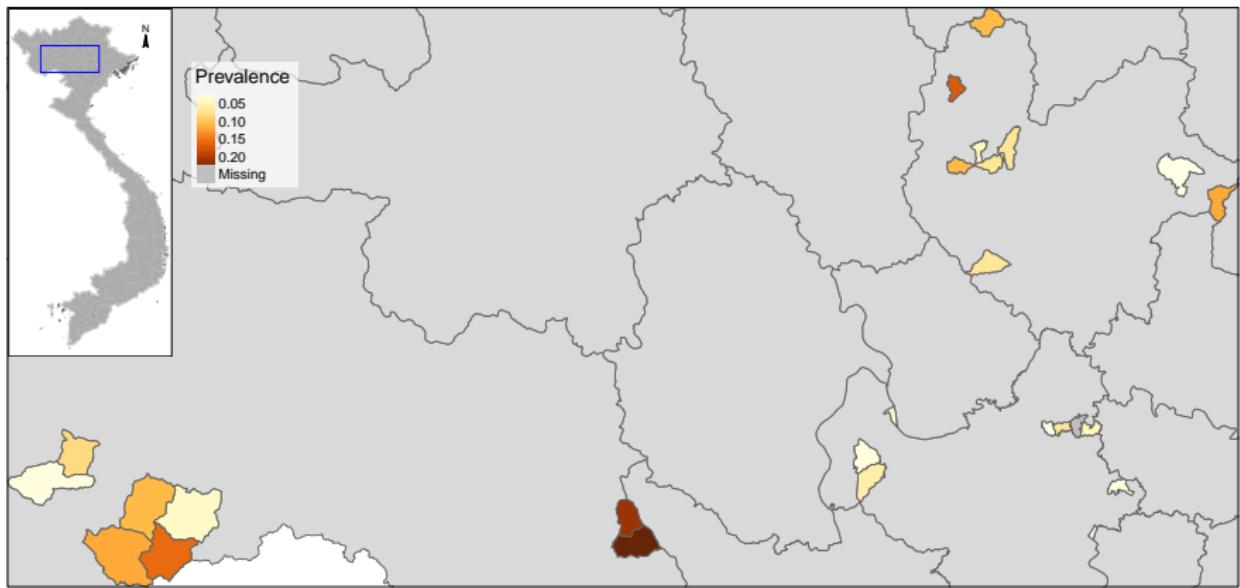


winter



spring

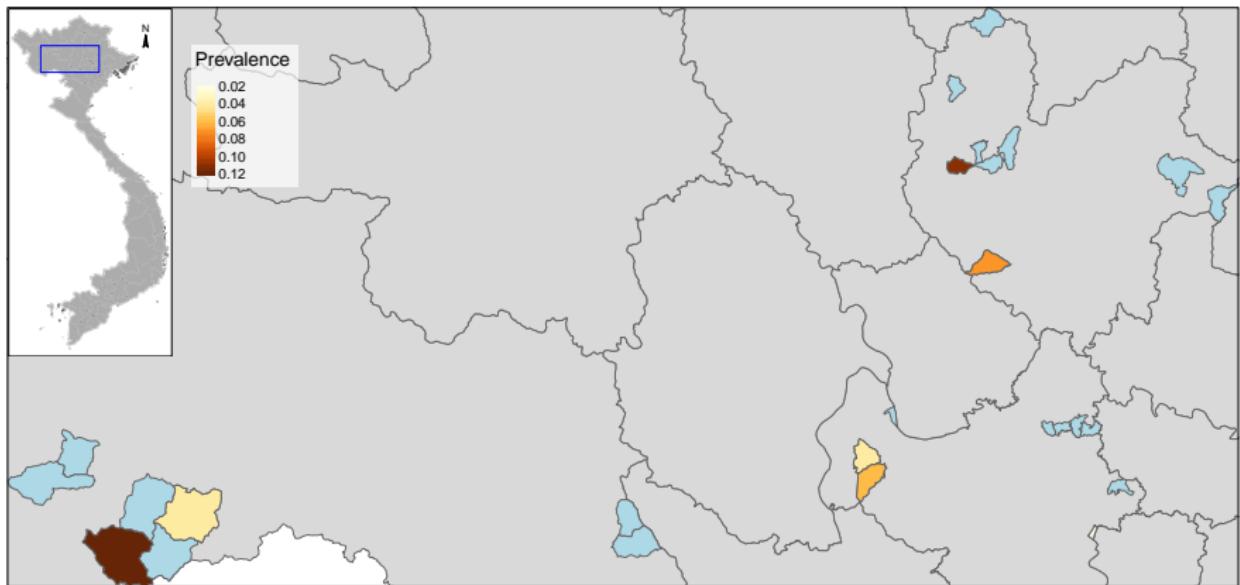




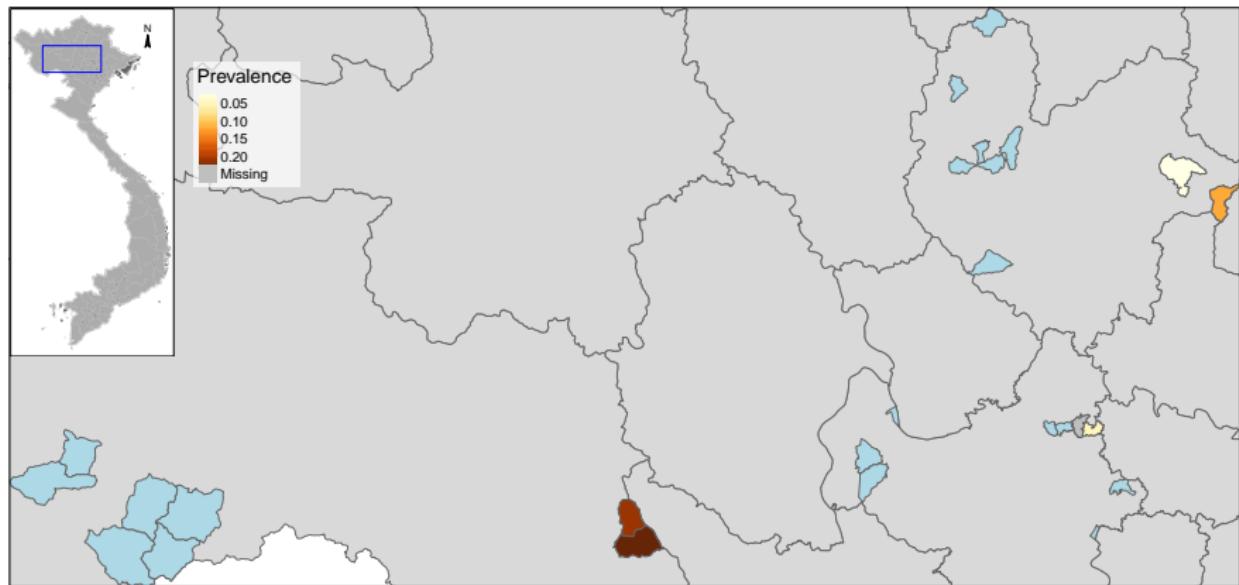
summer



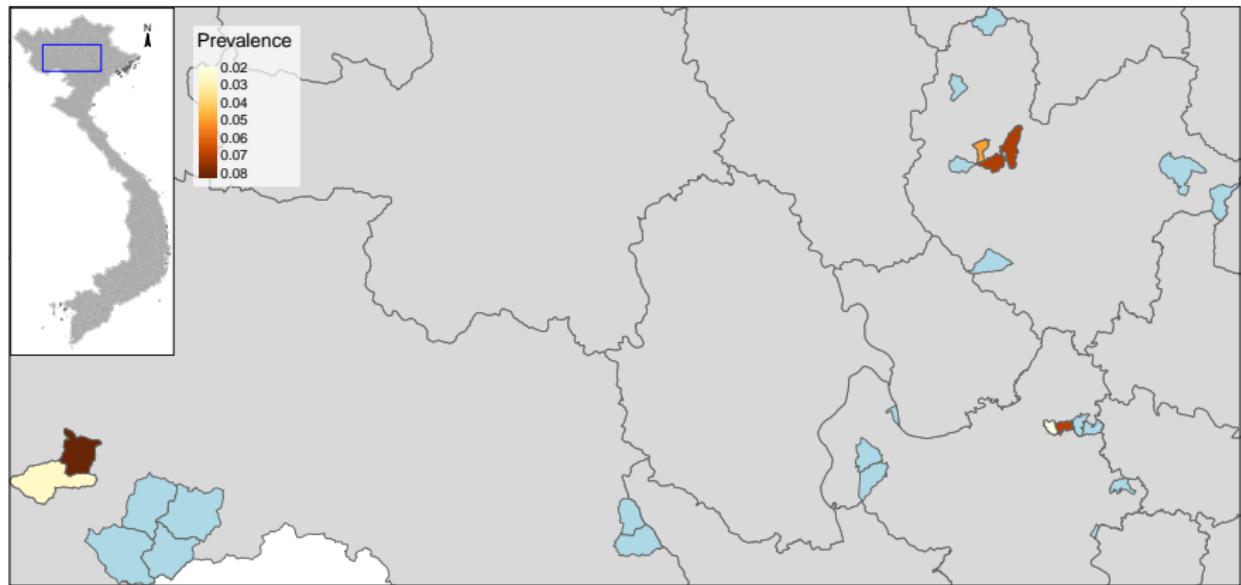
autumn



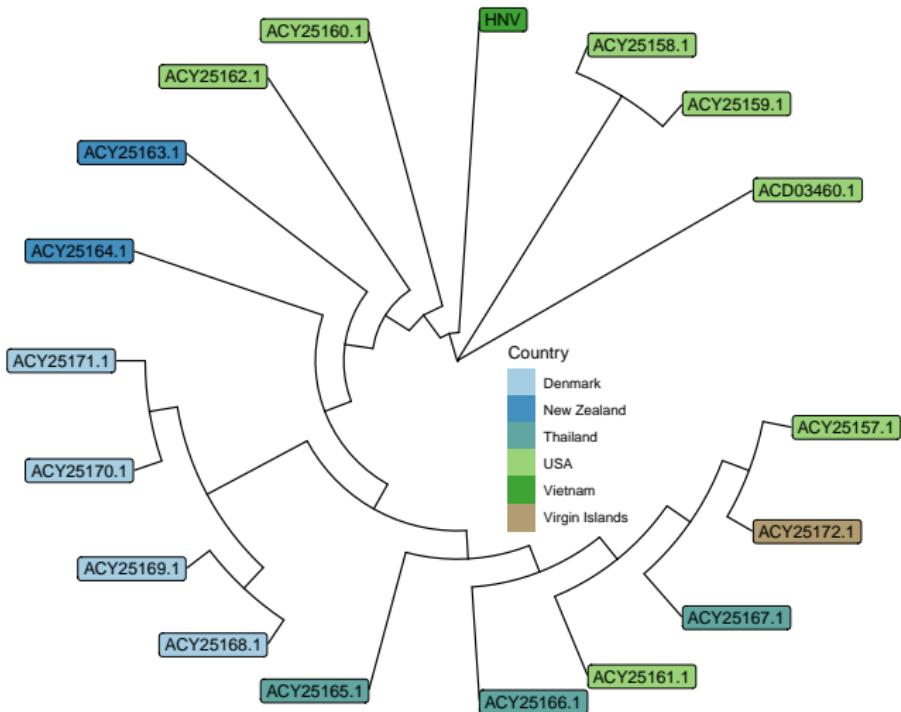
winter



spring



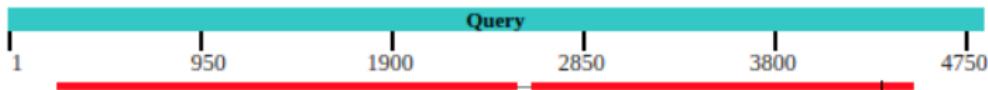
Assembly: 124,552 bp, 100 CDS (96 identified as the reference)  
DNA polymerase (identities: 966/979 (99%), gaps: 3/979 (0%))



HNV.07, 5 NAGY secret egész

Assembly: 4,841 bp (depth 520)

### Distribution of the top 3 Blast Hits on 1 subject sequences



*Haematobia irritans* densovirus isolate HiDV/URU, partial genome  
4,283 bp

Uruguay

Range 1: 43 to 2329, identities: 2112/2290(92%), gaps: 8/2290(0%)

Range 2: 2326 to 4056, identities: 1517/1734(87%), gaps: 6/1734(0%)

Range 3: 4109 to 4280, identities: 156/172(91%), gaps: 1/172(0%)

Sample	Contig	bp	Best match	Identities	Gaps
TNV_09	k59_7	239	Anaplasma marginale strain Jaboticabal	239/239 (100%)	0/239 (0%)
	k59_30	255	Anaplasma marginale strain Jaboticabal	255/255 (100%)	0/255 (0%)
HNV_07	k141_5	307	Trypanosoma vivax Y486	84/97 (87%)	7/97 (7%)
	k141_10	349	Leishmania amazonensis strain UA301	131/133 (98%)	0/133 (0%)
	k141_1	324	Leishmania donovani strain LdCL	257/306 (84%)	2/306 (0%)
	k141_7	512	Leishmania donovani strain LdCL	385/456 (84%)	0/456 (0%)
	k141_22	369	Trypanosoma vivax Y486	355/369 (96%)	0/369 (0%)
	k141_4	397	Leishmania donovani strain Dd8	321/382 (84%)	14/382 (3%)
	k141_14	742	Trypanosomatidae sp. GMO-05	580/581 (99%)	0/581 (0%)
	k141_18	1079	Trypanosoma kuseli	749/825 (91%)	19/825 (2%)
	k141_19	1168	Trypanosoma theileri YMG-11	1033/1141 (91%)	42/1141 (3%)
	k141_20	1662	Leptomonas pyrrhocoris	1519/1666 (91%)	5/1666 (0%)
	k141_21	3062	Trypanosomatidae sp. GMO-05	1114/1120 (99%)	1/1120 (0%)